

/organism="Heterosigma akashiwo"
/db_xref="taxon:2829"
/note="Isolated from red-tide sea water in Masan Bay,
Korea; classified by morphological studies"
<1..>712
/note="variable domains D1 and D2"
/product="24S large subunit ribosomal RNA"
BASE COUNT 164 a 149 c 211 g 188 t
ORIGIN

Query Match 100.0%; Score 23; DB 8; Length 712;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCACGACTGAGCAGCACCTTT 23
|||||
Db 149 ACCACGACTGAGCAGCACCTTT 127

RESULT 2
AF086948/c 713 bp DNA linear PLN 15-OCT-1998
LOCUS Heterosigma akashiwo large subunit ribosomal RNA gene, partial
SEQUENCE
AF086948
VERSION AF086948.1 GI:3695263
KEYWORDS
SOURCE Heterosigma akashiwo.
ORGANISM Heterosigma akashiwo
REFERENCE 1 (bases 1 to 713)
AUTHORS Eukaryota; stramenopiles; Raphidophyceae; Heterosigma.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1998) Environmental Conservation Division,
National Marine Fisheries Service, 2725 Montlake Blvd East,
Seattle, WA 98112, USA
FEATURES
source
1..713
/organism="Heterosigma akashiwo"
/strain="CCMP-452"
/db_xref="taxon:2829"
<1..>713
/note="contains variable domains D1-D3"
/product="large subunit ribosomal RNA"
BASE COUNT 165 a 148 c 210 g 190 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCACGACTGAGCAGCACCTTT 23
|||||
Db 147 ACCACGACTGAGCAGCACCTTT 125

RESULT 3
AF210741/c 715 bp DNA linear PLN 02-JAN-2001
LOCUS Heterosigma akashiwo large subunit ribosomal RNA gene, partial
DEFINITION
AF210741
VERSION AF210741.1 GI:12003313
KEYWORDS
SOURCE Heterosigma akashiwo.
ORGANISM Heterosigma akashiwo
REFERENCE 1 (bases 1 to 715)
AUTHORS Eukaryota; stramenopiles; Raphidophyceae; Heterosigma.
TITLE Tyrell,J.V., Scholin,C.A., Bergquist,P.R. and Bergquist,P.L.
JOURNAL Detection and Enumeration of Heterosigma akashiwo and Fibrocapsa
japonica (Raphidophyceae) Using rRNA-Targeted Oligonucleotide
Probes
UNPUBLISHED

REFERENCE 2 (bases 1 to 715)
AUTHORS Tyrell,J.V., Bergquist,P.R., Mackenzie,L. and Bergquist,P.L.
TITLE Phylogeny of the Raphidophytes Based on Large-Subunit rRNA Gene
Sequences
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 715)
AUTHORS Tyrell,J.V., Bergquist,P.R., Mackenzie,L. and Bergquist,P.L.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1999) Research and Development, Monterey Bay
Aquarium Research Institute, 7700 Sandholdt Road, Moss Landing, CA
95039-0628, USA
FEATURES
source
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/organism="Heterosigma akashiwo"
/strain="CAMR05"
/db_xref="taxon:2829"
<1..>715
/note="D1 and D2 domain"
/product="large subunit ribosomal RNA"
BASE COUNT 166 a 148 c 212 g 189 t
ORIGIN

Query Match 100.0%; Score 23; DB 8; Length 715;
Best Local Similarity 100.0%; Pred. No. 0.15;

QY 1 ACCACGACTGAGCAGCACCTTT 23
|||||
Db 149 ACCACGACTGAGCAGCACCTTT 127

RESULT 4
AF211256/c 715 bp DNA linear PLN 11-JAN-2001
LOCUS Heterosigma sp. CAMR10 large subunit ribosomal RNA gene, partial
DEFINITION
AF211256
VERSION AF211256
KEYWORDS
SOURCE AF211256.1 GI:12082493
ORGANISM Heterosigma sp. CAMR10.
REFERENCE 1 (bases 1 to 715)
AUTHORS Eukaryota; stramenopiles; Raphidophyceae; Heterosigma.
TITLE Tyrell,J.V., Scholin,C.A., Bergquist,P.R. and Bergquist,P.L.
JOURNAL Detection and Enumeration of Heterosigma akashiwo and Fibrocapsa
japonica (Raphidophyceae) Using rRNA-Targeted Oligonucleotides
UNPUBLISHED
REFERENCE 2 (bases 1 to 715)
AUTHORS Tyrell,J.V., Bergquist,P.R., Mackenzie,L. and Bergquist,P.L.
TITLE Phylogeny of the Raphidophytes Based on Large-subunit rRNA Gene
Sequences
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 715)
AUTHORS Tyrell,J.V., Bergquist,P.R., Mackenzie,L. and Bergquist,P.L.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-1999) Research and Development, Monterey Bay
Aquarium Research Institute, 7700 Sandholdt Road, Moss Landing, CA
95039-0628, USA
FEATURES
source
1..715
/organism="Heterosigma sp. CAMR10"
/strain="CAMR10"
/db_xref="taxon:147349"
/note="similar to Heterosigma akashiwo sequence AF210741"
<1..>715
/note="D1 and D2 domains; similar to Heterosigma akashiwo
sequence presented in GenBank Accession Number AF210741"
/product="large subunit ribosomal RNA"
BASE COUNT 166 a 148 c 212 g 189 t
ORIGIN

Query Match 100.0%; Score 23; DB 8; Length 715;
Best Local Similarity 100.0%; Pred. No. 0.15;

GenCore version 5.1.3
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OK nucleic - nucleic search, using sw model

Run on: October 17, 2002, 08:07:35 ; Search time 978.267 Seconds
(without alignments)
492.003 Million cell updates/sec

Title: US-09-780-113d-15
Perfect score: 23
Sequence: 1 accacgactgacgacacccctt 23

Scoring table: IDENTITY NDC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_da:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hgt_hum:*
31: em_hgt_inv:*
32: em_hgt_other:*
33: em_hgtg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Score | Match Length | DB ID | Description |
|------------|-------------|--------------|-------|-------------|
| 1. 712 | | | | |

| | | | | | | | |
|---|----|------|-------|--------|-----|------------|--------------------|
| c | 1 | 23 | 100.0 | 712 | 8 | AF042820 | AF042820 Heterosig |
| c | 2 | 23 | 100.0 | 713 | 8 | AF086948 | AF086948 Heterosig |
| c | 3 | 23 | 100.0 | 715 | 8 | AF210741 | AF210741 Heterosig |
| c | 4 | 23 | 100.0 | 715 | 8 | AF211256 | AF211256 Heterosig |
| c | 5 | 23 | 100.0 | 4103 | 8 | AF409124 | AF409124 Heterosig |
| c | 6 | 18.2 | 79.1 | 126149 | 9 | AC006352 | AC006352 Homo sapi |
| c | 7 | 18.2 | 79.1 | 169710 | 2 | AL627202 | AL627202 Homo sapi |
| c | 8 | 18.2 | 79.1 | 188930 | 2 | AL592114 | AL592114 Homo sapi |
| c | 9 | 18.2 | 79.1 | 187083 | 2 | AC091106 | AC091106 Mus muscu |
| c | 10 | 18.2 | 79.1 | 214025 | 2 | AC007882 | AC007882 Homo sapi |
| c | 11 | 18.2 | 79.1 | 227856 | 2 | AC007908 | AC007908 Homo sapi |
| c | 12 | 18.2 | 79.1 | 234542 | 9 | HUAC002041 | AC012495 Homo sapi |
| c | 13 | 17.8 | 77.4 | 215359 | 9 | CNS000VE | AL096607 Homo sapi |
| c | 14 | 17.4 | 75.7 | 34105 | 2 | AC021605 | AC021605 Homo sapi |
| c | 15 | 17.4 | 74.8 | 137764 | 2 | AL496629 | AL496629 Human DNA |
| c | 16 | 17.2 | 74.8 | 26889 | 9 | AC004791 | AL359434 Human DNA |
| c | 17 | 17.2 | 74.8 | 43772 | 9 | AL359434 | AC095461 Rattus no |
| c | 18 | 17.2 | 74.8 | 46708 | 9 | AC005363 | AC005363 Homo sapi |
| c | 19 | 17.2 | 74.8 | 73806 | 2 | AC005606 | AC005606 Homo sapi |
| c | 20 | 17.2 | 74.8 | 75108 | 9 | AE006640 | AE006640 Homo sapi |
| c | 21 | 17.2 | 74.8 | 80658 | 9 | AC074178 | AC005164 Homo sapi |
| c | 22 | 17.2 | 74.8 | 81579 | 9 | AC093758 | AC024947 Homo sapi |
| c | 23 | 17.2 | 74.8 | 107549 | 9 | AC004858 | AC004958 Homo sapi |
| c | 24 | 17.2 | 74.8 | 123331 | 9 | AC010539 | AC010539 Homo sapi |
| c | 25 | 17.2 | 74.8 | 128628 | 9 | AF069291 | AF069291 Homo sapi |
| c | 26 | 17.2 | 74.8 | 163031 | 9 | AC094935 | AC015679 Homo sapi |
| c | 27 | 17.2 | 74.8 | 163889 | 2 | AC024947 | AC093758 Mus muscu |
| c | 28 | 17.2 | 74.8 | 175996 | 2 | AF117829 | AF117829 Homo sapi |
| c | 29 | 17.2 | 74.8 | 184919 | 2 | AC109793 | AC109793 Bos tauru |
| c | 30 | 17.2 | 74.8 | 207962 | 2 | AC094935 | AC094935 Rattus no |
| c | 31 | 17.2 | 74.8 | 238169 | 2 | HSCRMPO6 | AF096145 Homo sapi |
| c | 32 | 17.2 | 74.8 | 242965 | 2 | AF349055 | AF349055 Unculture |
| c | 33 | 17.2 | 74.8 | 320250 | 9 | AC100075 | AC100075 Mus muscu |
| c | 34 | 17 | 73.9 | 154921 | 2 | AC105915 | AC105915 Homo sapi |
| c | 35 | 17 | 73.9 | 205140 | 2 | AC005079_2 | Continuation (3 of |
| c | 36 | 17 | 73.9 | 335372 | 2 | AL137860 | AL137860 Homo sapi |
| c | 37 | 16.8 | 73.0 | 38780 | 2 | AC022529 | AC022529 Homo sapi |
| c | 38 | 16.8 | 73.0 | 42856 | 355 | AC005059 | AC005059 Homo sapi |
| c | 39 | 16.8 | 73.0 | 42856 | 13 | AC094641 | AC094641 Rattus no |
| c | 40 | 16.8 | 73.0 | 110000 | 2 | | |
| c | 41 | 16.8 | 73.0 | 110000 | 2 | | |
| c | 42 | 16.8 | 73.0 | 121459 | 2 | | |
| c | 43 | 16.8 | 73.0 | 168042 | 2 | | |
| c | 44 | 16.8 | 73.0 | 170128 | 2 | | |
| c | 45 | 16.8 | 73.0 | 175390 | 2 | | |

ALIGNMENTS

RESULT 1
LOCUS AF042820/c 712 bp DNA linear PIN 01-FEB-1998
DEFINITION Heterosigma akashiwo 24S large subunit ribosomal RNA gene, partial
ACCESSION AF042820
VERSION AF042820.1 GI:2827390
KEYWORDS
SOURCE Heterosigma akashiwo.
ORGANISM Heterosigma akashiwo
REFERENCE 1 (bases 1 to 712)
AUTHORS Lee,S.W., Park,C.G. and Park,Y.S.
TITLE 24S ribosomal RNA sequence analysis of dinoflagellates isolated from red-tide in southern coast of Korea
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 712)
AUTHORS Lee,S.W., Park,C.G. and Park,Y.S.
TITLES Direct Submission
JOURNAL Submitted (14-JAN-1998) Department of Microbiology, Inje University, Obangdong 607, Kimhae 621-749, Korea
FEATURES
source 1..712